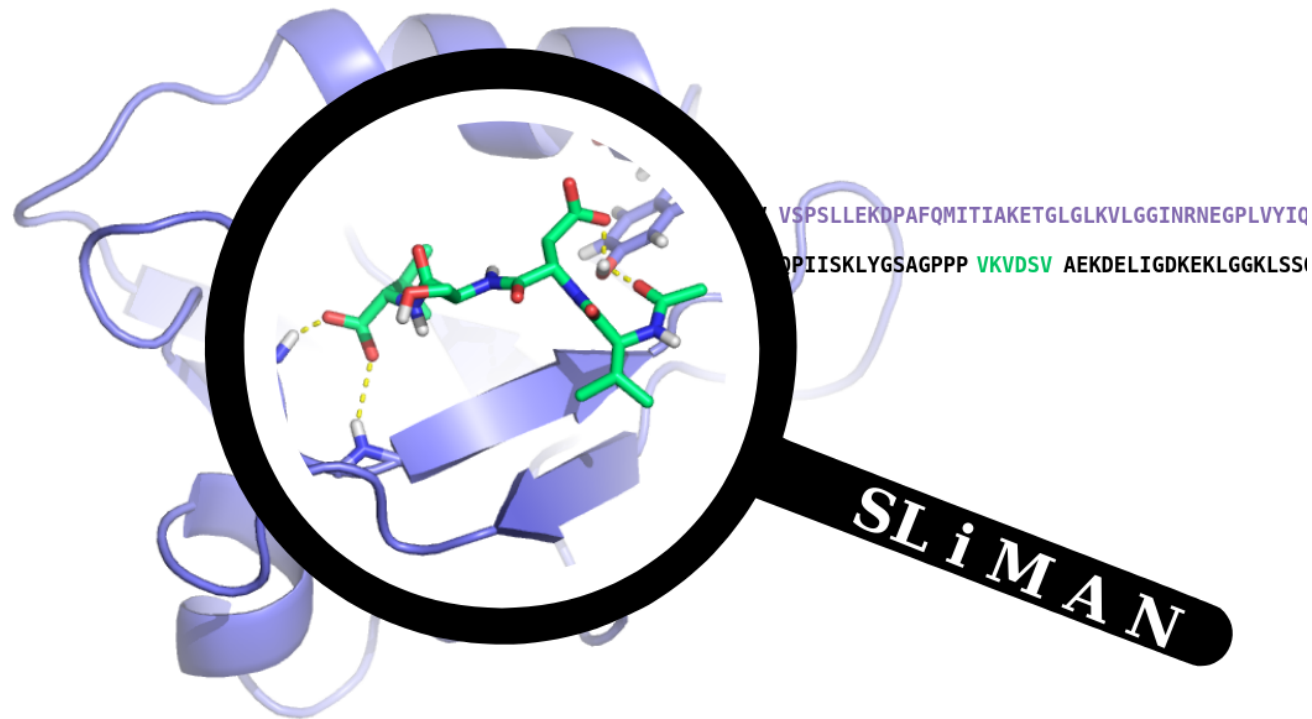


SLiMAN - Instruction manual

Version 2.0



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SLiMAN - Inputs

New SLiMAN Project

Project Name

MyNewProject

Give a name *to your project (optional)*

Uniprot File No file selected.

Load an input file (ex : [InputFile.txt](#))

And / Or

And/Or (Inputs can be combined)

Uniprot List (must be separated by comma)

BRAF_HUMAN, 1433S_HuMAN, 1433Z_HUMAN

Provide a list of protein names **separated by commas** *

Open Access

Make your project accessible to others (or not)

Find Interactions

Launch SLiMAN !

* Note : *only uniprot ACC and ID are accepted*

SLiMAN - Running query

LiMIP

Linear Motif Interaction Prediction

Estimated computation time required for your request : 19 seconds

Expected Computation time left : 10 seconds

Your results will be available at this

LINK

INPUT NOTES :

Project Name : **MyNewProject**

Results Accessibility : Open Access

Results URL : http://sliman.cbs.cnrs.fr/LiMIP/result_request.py?user_id=MyNewProject

Creation time : 2021-03-02 16:11:36

LiMIP version : 2.0

INPUT UNIPROT LIST :

P15056, P31947, P63104

Total Unicode found : 3

← Time estimation for completion

← Link to results

← The project name : Name allowing results accessibility

← Project accessibility : 'Open access' or 'Hidden' *

← Absolute results URL : Share this URL with collaborators to work on the same project

← SLiMIP Version

← Accepted entries summary : Displayed validated protein entries used for the project

* Note : In open access mode, SLiMAN results will be displayed in the 'Webserver results' section

SLiMIP - Result table

ELM ANALYSIS: ELM motifs are displayed as rows in the table

PFam columns: Pfam domains displayed as columns in the table

PFam protein entry

| ELM ANALYSIS | | | | | FILTERED UNIPROT LIST | |
|--------------|--------------------|--------|----------|--|-----------------------|-------------------|
| | | | | | 1433S_HUMAN | 1433Z_HUMAN |
| | | | | | P31947 | P63104 |
| UNIPROT | ELM_Class | Motif | Location | Class_RegEx | PF00244 14-3-3 | PF00244 14-3-3 |
| BRAF_HUMAN | LIG_14-3-3_CanoR_1 | RSSSAP | 362-367 | R[[^] DE]{0,2}[[^] DEPG]([ST]) (([^] [FWYLMV].) ([^] [PRIKGN]P) ([^] [PRIKGN].{2,4}[VILMFWYP])) | Alignments(93) | Alignments(93) |
| P15056 | LIG_14-3-3_CanoR_1 | RMKTLG | 437-442 | R[[^] DE]{0,2}[[^] DEPG]([ST]) (([^] [FWYLMV].) ([^] [PRIKGN]P) ([^] [PRIKGN].{2,4}[VILMFWYP])) | Alignments(93) | Alignments(93) |

SLiMID Alignment :
Link to SLiMID alignments.

- 93 templates are available for this Hit alignments.
(‘No Templates’ could also be a value)

ELM protein entry

Motif boundaries : Start and end location of the motif on the sequence.

Protein motif : Matched motif of the ELM class.

ELM classes : List of the matched elm classes of the protein entry.

ELM class RegEx : Regular Expression put to use to parse and find the corresponding motif on the sequence.

SLiMIP hit: BRAF LIG_14-3-3 motif linked to 1433S domain.
- Coloring scheme related to ‘confidence level’.

- Number of 3D template available.
- While hovering over the hit, detailed information are displayed : BioGRID, IUpred, ELM & SLiMID

SLiMIP - Parameters

| Parameters Panel | | | |
|------------------|--------------------------|--|--|
| Parameter | Actual Set | Modify | |
| ELM | Motif E-value | <=0.005 | <input type="text" value="0.005"/> |
| | Verified Instances | NO | <input type="checkbox"/> |
| | Class Types | MOD = YES DOC = YES LIG = YES DEG = YES TRG = YES CLV = YES | <input checked="" type="checkbox"/> MOD <input checked="" type="checkbox"/> DOC <input checked="" type="checkbox"/> LIG <input checked="" type="checkbox"/> DEG <input checked="" type="checkbox"/> TRG <input checked="" type="checkbox"/> CLV |
| IUpred | Strict disorder | NO | <input type="checkbox"/> |
| | Short avg_score | >= 0.3 | <input type="range" value="0.30"/> |
| | Long avg_score | >= 0.3 | <input type="range" value="0.30"/> |
| | Short Glob_Dom avg_score | >= 1.0 | <input type="range" value="1.00"/> |
| | Long Glob_Dom avg_score | >= 0.0 | <input type="range" value="0.00"/> |
| | ANCHOR2 avg_score | >= 0.5 | <input type="range" value="0.50"/> |
| BioGrid | Low Throughput | >= 0 | <input type="text" value="0"/> |
| | High Throughput | >= 0 | <input type="text" value="0"/> |
| | Total count | >= 1 | <input type="text" value="1"/> |
| Confidence | Level | >= 1 | <input type="text" value="1"/> |
| SLiMID | Nb Templates | >= 0 | <input type="text" value="0"/> |
| SLiMIM | Validated Models | >= 0 | <input type="text" value="0"/> |
| Sorting | Algorithm | Original Input Order | <input type="radio"/> Alphabetic <input checked="" type="radio"/> InputOrder <input type="radio"/> Clusters |
| User Action | | <input type="button" value="Default"/> <input type="button" value="Reset"/> <input type="button" value="Update Parameters"/> | |

ELM E-value: Probability to find by coincidence.
(The lower the better).

ELM verified instances: Is the hit within ELM verified instances database ?

ELM class types: Check class types to be displayed.

Mod = Post-translational modification

Doc = Docking site

Lig = Ligand binding site

Deg = Degradation site

Trg = Targeting site

Clv = Cleavage site

IUpred Strict-disorder: Are all a.a of the motif >0,5 for all Short, ShotGlob and Anchor2 scores ?

IUpred disorder scores: Filter out IUpred scores below the selected thresholds.

BioGRID interactions count: Check numbers of interactions (between protein pairs).

SLiMIP hit confidence: Check hit has a confidence level above threshold.

Note : Refere to confidence table color codes

SLiMID available templates : Check if hits match a given number of SLiMID templates.

SLiMIM validated models: Check if hits have validated models above threshold.

Sorting Algorithm: Ordering proteins displayed in the table.

Set default parameters

Update Parameters : Once parameters have been changed, update the page.

SLiMID - Segmentation

Template alignments

ELM match : BRAF_HUMAN (P15056) - LIG_14-3-3_CanoR_1

- Parsing Regex : R[[^]DE]{0,2}[[^]DEPG]([ST])((FWYLMV).)|([[^]PRIKGN]P)|([[^]PRIKGN].{2,4}{VILMFWYP}))
- Class E-value : 0.0044766733275

ELM match summary

Highlighted matched ELM motif

```
MAALSGGGGGGAEPGQALFNGDMEPEAGAGAGAAAADPAIPPEEWNKQMIKLTQEHEIALDKFGEHNPPSIYLEAYEETSCLDALQREQLLES LGNGTDFSVSSASMDVTSSSSSLVLPSSLVFNPTDVARSNPKSPQKPIVRFVLPNKQRTVVPARCGVTVRDSLKALMMRGLIPECCAVYRIQDGE  
KQPIGWDTDISWLTGEEHVEVLENVPLTTHNFVRKTFFTLAFCDPCRLLFGFRQCCTCGYKFHQRCEVPLMVCVNYDQLDLFVSKFFEHPHQEEASLAETALTSGSSPSAPASDSIGPQILTSPPSPKSIPIPPFRPAEDHRNQFGRDRSSSAFNVHINTIEPVNIDD LIRDQGFRGDGSGTTGLSATPPASLP6  
SLTNVKALQKSPGPRERKSSSSSEDNRNMTLGRDSSDDWEIPDGGITVGGQRIQSGSFGTVYKKGWHDVAVKMLHVTAPTQQQLQAFKNEVGVLRKTRHVHILLFMGYSTKPKQLAIVTQWCEGSSLYHHLHIETKFEHIKLIIDARQTAQGM DYLHAKSIIHRDLKSNHIFLHEDLTVKIGDFGLATVKSRSWSGSHQFEQ  
LSGSILWMAPEVIRMQDKNPYSFQSDVYAFGIVLYELMTGQLPYSINNRDQIIFHVGRGYLSPDLSKVRSNCPKAMKRLMAECLKKRDERPLFPQILASIELLARS LPKIHRSASEPSLNRAGFQTEDFS LYACASPKTPIQAGGYGAFPVH
```

ELM RegEx segmentation : from 362 to 367

Original segmentation
by ELM

Full ELM protein sequence

Motif Segmentation : From To

Motif segmentation: User can modify the motif boundaries.

Note : Click the 'Update alignment' button after boundaries modification to update corresponding alignments.

PFam match : 1433S_HUMAN (P31947) - PF00244 - 14-3-3

Pfam protein match summary

```
MERASLIQKAKLAEQAERYEDHAAPHKGAVEKGEELSCERNLLSVAYKNVVGQRAAWRVLSSIEQKSNEEGSEEKGEVREYREKVELQGVCDTVLGLLDSHLIKEAGDAESRVFLKHKGDYRYLAEVATGDDKKRIIDSARSAYQEANDISKKEPPTHPPIRGLALNFSVFHYEIANSPPEEAI SLAKTTFDEAMAD  
LHTLSEDSYKDDSTLIMQLRDNLTLWTADNAGEEGGEAPQEPQS
```

PFam Data : Domain segmentation from 9 to 231

Original segmentation
by PFam

Full PFam protein
sequence

Highlighted current
domain segmentation

Modify Domain Segmentation : From To

Update alignment with current domain segmentation

Domain segmentation: User can modify the domain boundaries.

Note : Click the 'Update alignment' button after boundaries modification to update corresponding alignments.

Update alignment button: Apply current segmentation to sequence-structure alignments.

SLiMID - Alignments

Query Peptide Motif(s) : RSSSAP ← **Peptide query:** Aligned peptide
Query Pfam Sequence :
 KAKLAEQAERYEDMAAFMKGAVEKGEELSCEERNLLSVAYKNVGGQRAAWRVLSSIEQKSNEEGSEEKGPEVREYREKVVETELQGVCDTVGLLDShLIKEAGDAESRVFYLKMKGDYRYLAEVATGDDKKRIIDSARSAYQEAMDISKEMPPTNPIRLGLALNFSVFHYEIANSP EEAISL
 TTFDEAMADLHTLSEDSYKDSLIMQLLRDNLTLWT ← **Domain query:** Aligned domain sequence
Selected Templates :
 3IQJ_A_complex_peptide_256_261_P.pdb
 Launch Modeling ! ← **Selected templates list:** Summary of the selected models to be used for modeling

Global selector: select all available templates

Template resolution

Identity highlight: Strict conservation is highlighted

SLiMIM modeling query: Submit modeling with selected alignments and templates.

| Selector | PDB ID | Entry | Reso A | Motif | ChainID | %Ident | %QueryCov | Nb Contacts | Peptide alignment: query (top) vs template (bottom). |
|-------------------------------------|--------|---------------------------|--------|--------|---------|--------|----------------|-------------|--|
| | | | | Domain | | | | | |
| <input type="checkbox"/> | 5LU2 | 5LU2_A_cPep_1_3_18_D.pdb | 2.5 | ELM | D | 66.7 | 100.0 100.0 | 18 100.0 | -RSSSAP -RRASAP -----KAKLAEQAERYEDMAAFMKGAVEKGEELSCEERNLLSVAYKNVGGQRAAWRVLSSIEQKSNEEGSEEKGPEVREYREKVVETELQGVCDTVGLLDShLI ERASLIQKAKLAEQAERYEDMAAFMKGAVEKGEELSCEERNLLSVAYKNVGGQRAAWRVLSSIEQKSNEEGSEEKGPEVREYREKVVETELQGVCDTVGLLDShLI |
| <input checked="" type="checkbox"/> | 3IQJ | 3IQJ_A_cPep_256_261_P.pdb | 1.15 | ELM | P | 66.7 | 100.0 100.0 | 18 100.0 | -RSSSAP -RSTSTP -----KAKLAEQAERYEDMAAFMKGAVEKGEELSCEERNLLSVAYKNVGGQRAAWRVLSSIEQKSNEEGSEEKGPEVREYREKVVETELQGVCDTVGL GANGSMERASLIQKAKLAEQAERYEDMAAFMKGAVEKGEELS - EERNLLSVAYKNVGGQRAAWRVLSSIEQKSNEEGSEEKGPEVREYREKVVETELQGVCDTVGL |

SLiMAN link of the template
 Note : Click to download

PDB link to template structure

Template selector : Check it to use this template for modeling

Contacts coloring: Residues in contacts with the ELM motif are colored:
 Green < 4 Å
 Yellow < 5,5 Å
 Red < 7 Å

Domain alignment: query (top) vs template (bottom).

SLiMIM - Models

Discarded: List of discarded models.

Note : After saving, discarded models will be deleted from the project.

Discarded

- P31947_PF00244_by_3IQJ_A_complex_peptide_256_261_P/SCWRL/BLAST

Link to download all models as zip archive

-> Download Analysis.zip  <-

Validated: List of validated models.

Note : Validated models are forwarded to SLiMIP results and is also a filter-parameter.

Validated

- P31947_PF00244_by_5LU2_A_complex_peptide_13_18_D/SCWRL/BLAST
- P31947_PF00244_by_5LU2_A_complex_peptide_13_18_D/SCWRL/MAFFT

Save Selection

Selection update:

After model selection, click the button to save and forward the data to SLiMIP.


































Model validations: Check the appropriate button to discard or validate models.

Note : Can be left unselected

Currently displayed model : A 'green eye' is displayed on the row of the currently visualized structure.

Modeling software

Alignment software

| | PDB | SLiMID | Reso. | %Ident | Software | Alignment | PFam Domain Model | Motifs | Peptide Model | Complexes | Validation |
|--|---|--|-------|--------|----------|-----------|--|-------------------|--|--|--|
|  | 5LU2  | 5LU2_A_complex_peptide_13_18_D  | 2.5 | 100.0 | SCWRL | BLAST | MODEL  TEMPLATE  FASTA  | -RSSAP -RRASAP | MODEL  TEMPLATE  FASTA  | COMPLEXE  | <input type="radio"/> <input type="radio"/> <input checked="" type="radio"/> |
| | | | | | | MAFFT | MODEL  TEMPLATE  FASTA  | -RSSAP -RRASAP | MODEL  TEMPLATE  FASTA  | COMPLEXE  | <input type="radio"/> <input type="radio"/> <input checked="" type="radio"/> |
| | 3IQJ  | 3IQJ_A_complex_peptide_256_261_p  | 1.1 | 99.5 | SCWRL | BLAST | MODEL  TEMPLATE  FASTA  | -RSSAP -RSTSTP | MODEL  TEMPLATE  FASTA  | COMPLEXE  | <input checked="" type="radio"/> <input type="radio"/> <input type="radio"/> |
| | | | | | | MAFFT | MODEL  TEMPLATE  FASTA  | -RSSAP -RSTSTP | MODEL  TEMPLATE  FASTA  | COMPLEXE  | <input type="radio"/> <input checked="" type="radio"/> <input type="radio"/> |

SLiMID template : Visualize or download the extracted SLiMID template

Original PDB structure : Visualize, download or access the original structure

Validated

Unselected

Discarded

SLiMAN BioGRID extention input

BioGrid Extention

Uniprot File No file selected.

Load input file (ex : [InputFile.txt](#))

And / Or

And/Or → One or both input are accepted

Uniprot List (must be separated by comma)

Write proteins list **separated by commas** *

Minimum number of interactions

Interaction count lower-boundary threshold


Launch SLiMAN-BioGRID extention !


* Note : only uniprot ACC and ID are accepted

BioGRID extension results

SLiMAN BioGrid Extension Results table

Threshold manager : modify threshold to filter out less frequent interactors.

Interactions threshold \geq 

| | | |
|---|---|---|
| SLiMAN QuickLaunch Query | <input type="text" value="Query Uniprot ID"/> <input type="text" value="All BioGrid Interactants Uniprot ID"/> | ← Uniprot ID : NAME_SPECIE (e.g. FRAT2_HUMAN) |
| | <input type="text" value="Query Uniprot ACC"/> <input type="text" value="All BioGrid Interactants Uniprot ACC"/> | ← Uniprot ACC : 6 letters Uniprot accession code (e.g. O75474) |
|  Quick Launch | <input type="text" value="FRAT2_HUMAN"/> <input type="text" value=" ,PTN12_HUMAN ,BUB1_HUMAN ,CTNA1_HUMAN ,GSK3B_HUMAN ,MLH3_HUMAN ,CDN2A_HUMAN ,EGFR_HUMAN ,XPO1_HUMAN ,MLH1_HUMAN ,RASN_HUMAN ,ERBB2_HUMAN ,CRCM_HUMAN ,RASK_HUMAN"/> | |
| | <input type="text" value="O75474"/> <input type="text" value=" ,Q05209 ,O43683 ,P35221 ,P49841 ,Q9UHC1 ,P42771 ,P00533 ,O14980 ,P40692 ,P01111 ,P04626 ,P23508 ,P01116"/> | |

Interactants entries: List of interactors in BioGRID database

Query entry: The query is displayed in first place

'Quick Launch' button: Send the **displayed** proteins into a new SLiMAN query.